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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=2; day=15; hr=12; min=18; sec=18; ms=279;]

=====

Reviewer Comments:

<400> 3

Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile
1 5 10 15

Trp Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln

20

25

30

Please remove the blank line between the amino acids and their respective numbers above. This error appears in subsequent amino acid sequences. Also, please remove the blank lines between rows of nucleotides (this appears in subsequent sequences).

(end of Sequence 86)

ttttatttta tttatttttt gatggagtc tgcaactccag cctggtgaca gact 1914

PF-1506 PCT

1/94

WASH_1695548.1

Please remove the above three lines of text, which appear at the end of the submitted file.

Application No: 10554917 Version No: 1.0

Input Set:**Output Set:**

Started: 2008-02-14 12:58:35.910
Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (7)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (13)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (15)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (16)

Input Set:

Output Set:

Started: 2008-02-14 12:58:35.910
Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (24)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (29)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31) POS (915)
E 330	Invalid protein , found in SEQID(86) POS (1) Invalid Protein:PCT

Input Set:

Output Set:

Started: 2008-02-14 12:58:35.910
Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
W 112	Upper case found in data; Found at position(1914) SeqId(86)
W 112	Upper case found in data; Found at position(1915) SeqId(86)
W 112	Upper case found in data; Found at position(1916) SeqId(86)
W 112	Upper case found in data; Found at position(1917) SeqId(86)
E 259	Found undefined lettercode; POS (1919) SEQID(86)
E 259	Found undefined lettercode; POS (1920) SEQID(86)
E 259	Found undefined lettercode; POS (1921) SEQID(86)
E 259	Found undefined lettercode; POS (1922) SEQID(86)
E 259	Found undefined lettercode; POS (1923) SEQID(86)
E 259	Found undefined lettercode; POS (1924) SEQID(86)
E 259	Found undefined lettercode; POS (1925) SEQID(86)
E 259	Found undefined lettercode; POS (1926) SEQID(86)
E 259	Found undefined lettercode; POS (1927) SEQID(86)
E 254	The total number of bases conflicts with running total, Input: 1, Calculated : 1927 SEQID(86)
E 253	The number of bases differs from <211> Input: 1914 Calculated:1927 SEQID (86)

<110> INCYTE CORPORATION; ELLIOTT, Vicki S.;
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HAFALIAL, April J.A.; BECHA, Shanya D.;
CHAWLA, Narinder K.; BAUGHN, Mariah R.;
LEE, Soo Yeun; TRAN, Uyen K.;
YUE, Henry; NGUYEN, Danniel B.;
THORNTON, Michael B.; GURURAJAN, Rajagopal;
GANDHI, Ameena R.; LU, Yan;
YAO, Monique G.; LI, Joana X.;
LUO, Wen; LEE, Ernestine A.;
FORSYTHE, Ian J.; ISON, Craig H.;
WILSON, Amy D.; JIN, Pei

<120> KINASES AND PHOSPHATASES

<130> PF-1506 PCT

<140> 10554917
<141> 2008-02-14

<150> US 60/467,491
<151> 2003-04-30

<150> US 60/469,441
<151> 2003-05-09

<150> US 60/476,408
<151> 2003-06-05

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<211> 83
<212> PRT
<213> Homo sapiens

<220>
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1 5 10 15
Asn Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu
20 25 30

Asp Gly Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Thr Thr
35 40 45
Trp Leu Ser Leu Cys Thr Ala Met Ser Pro Leu Thr Thr Glu Ile
50 55 60
Trp Ala Leu Arg Arg Gly Asn Ser Ser Ala Ser Trp Ser Arg Ala
65 70 75
Ala Ser Gly Gly Arg Arg Ser Pro
80

<210> 2

<211> 292

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7520272CD1

<400> 2

Met Ala Asp Gln Ala Pro Phe Asp Thr Asp Val Asn Thr Leu Thr
1 5 10 15
Arg Phe Val Met Glu Glu Gly Arg Lys Ala Arg Gly Thr Gly Glu
20 25 30
Leu Thr Gln Leu Leu Asn Ser Leu Cys Thr Ala Val Lys Ala Ile
35 40 45
Ser Ser Ala Val Arg Lys Ala Gly Ile Ala His Leu Tyr Gly Ile
50 55 60
Ala Gly Ser Thr Asn Val Thr Gly Asp Gln Val Lys Lys Leu Asp
65 70 75
Val Leu Ser Asn Asp Leu Val Met Asn Met Leu Lys Ser Ser Phe
80 85 90
Ala Thr Cys Val Leu Val Ser Glu Glu Asp Lys His Ala Ile Ile
95 100 105
Val Glu Pro Glu Lys Arg Gly Lys Tyr Val Val Cys Phe Asp Pro
110 115 120
Leu Asp Gly Ser Ser Asn Ile Asp Cys Leu Val Ser Val Gly Thr
125 130 135
Ile Phe Gly Ile Tyr Arg Lys Lys Ser Thr Asp Glu Pro Ser Glu
140 145 150
Lys Asp Ala Leu Gln Pro Gly Arg Asn Leu Val Ala Ala Gly Tyr
155 160 165
Ala Leu Tyr Gly Ser Ala Thr Met Leu Val Leu Ala Met Asp Cys
170 175 180
Gly Val Asn Cys Phe Met Leu Asp Pro Asp Asn Ser Ala Pro Tyr
185 190 195
Gly Ala Arg Tyr Val Gly Ser Met Val Ala Asp Val His Arg Thr
200 205 210
Leu Val Tyr Gly Gly Ile Phe Leu Tyr Pro Ala Asn Lys Lys Ser
215 220 225
Pro Asn Gly Lys Leu Arg Leu Leu Tyr Glu Cys Asn Pro Met Ala
230 235 240
Tyr Val Met Glu Lys Ala Gly Gly Met Ala Thr Thr Gly Lys Glu
245 250 255
Ala Val Leu Asp Val Ile Pro Thr Asp Ile His Gln Arg Ala Pro
260 265 270
Val Ile Leu Gly Ser Pro Asp Asp Val Leu Glu Phe Leu Lys Val
275 280 285

Tyr Glu Lys His Ser Ala Gln

290

<210> 3

<211> 434

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7521279CD1

<400> 3

Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile

1 5 10

15

Trp Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln

20 25 30

Arg Gly Val Cys Met Thr Asn Cys Pro Thr Leu Ile Val Met Val
35 40 45

Gly Leu Pro Ala Arg Gly Lys Thr Tyr Ile Ser Lys Lys Leu Thr
50 55 60

Arg Tyr Leu Asn Trp Ile Gly Val Pro Thr Arg Glu Phe Asn Val
65 70 75

Gly Gln Tyr Arg Arg Asp Val Val Lys Thr Tyr Lys Ser Phe Glu
80 85 90

Phe Phe Leu Pro Asp Asn Glu Glu Gly Leu Lys Ile Arg Lys Gln
95 100 105

Cys Ala Leu Ala Ala Leu Arg Asp Val Arg Arg Phe Leu Ser Glu
110 115 120

Glu Gly Gly His Val Ala Val Phe Asp Ala Thr Asn Thr Thr Arg
125 130 135

Glu Arg Arg Ala Thr Ile Phe Asn Phe Gly Glu Gln Asn Gly Tyr
140 145 150

Lys Thr Phe Phe Val Glu Ser Ile Cys Val Asp Pro Glu Val Ile
155 160 165

Ala Ala Asn Ile Val Gln Val Lys Leu Gly Ser Pro Asp Tyr Val
170 175 180

Asn Arg Asp Ser Asp Glu Ala Thr Glu Asp Phe Met Arg Arg Ile
185 190 195

Glu Cys Tyr Glu Asn Ser Tyr Glu Ser Leu Asp Glu Asp Leu Asp
200 205 210

Arg Asp Leu Ser Tyr Ile Lys Ile Met Asp Val Gly Gln Ser Tyr
215 220 225

Val Val Asn Arg Val Ala Asp His Ile Gln Ser Arg Ile Val Tyr
230 235 240

Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys
245 250 255

Arg His Gly Glu Ser Glu Leu Asn Leu Lys Gly Arg Ile Gly Gly
260 265 270

Asp Pro Gly Leu Ser Pro Arg Gly Arg Glu Phe Ala Lys Ser Leu
275 280 285

Ala Gln Phe Ile Ser Asp Gln Asn Ile Lys Asp Leu Lys Val Trp
290 295 300

Thr Ser Gln Met Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly
305 310 315

Val Pro Tyr Glu Gln Trp Lys Val Leu Asn Glu Ile Asp Ala Ser

320	325	330
Tyr Glu Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu		
335	340	345
Glu Arg Gln Glu Asn Val Leu Val Ile Cys His Gln Ala Val Met		
350	355	360
Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ala Ala Glu Gln Leu		
365	370	375
Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu Thr Pro		
380	385	390
Val Ala Tyr Gly Cys Lys Val Glu Ser Ile Phe Leu Asn Val Ala		
395	400	405
Ala Val Asn Thr His Arg Asp Arg Pro Gln Asn Val Asp Ile Ser		
410	415	420
Arg Pro Pro Glu Glu Ala Leu Val Thr Val Pro Ala His Gln		
425	430	

<210> 4

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7523965CD1

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20	25	30
Arg Val Leu Ser Gly Asp Leu Gly Gln Leu Pro Thr Gly Ile Arg		
35	40	45
Asp Phe Val Glu His Ser Ala Arg Leu Cys Gln Pro Glu Gly Ile		
50	55	60
His Ile Cys Asp Gly Thr Glu Ala Glu Asn Thr Ala Thr Leu Thr		
65	70	75
Leu Leu Glu Gln Gln Gly Leu Ile Arg Lys Leu Pro Lys Tyr Asn		
80	85	90
Asn Cys Trp Leu Ala Arg Thr Asp Pro Lys Asp Val Ala Arg Val		
95	100	105
Glu Ser Lys Thr Val Ile Val Thr Pro Ser Gln Arg Asp Thr Val		
110	115	120
Pro Leu Pro Pro Gly Gly Ala Arg Gly Gln Leu Gly Asn Trp Met		
125	130	135
Ser Pro Ala Asp Phe Gln Arg Ala Val Asp Glu Arg Phe Pro Gly		
140	145	150
Cys Met Gln Gly Arg Thr Met Tyr Val Leu Pro Phe Ser Met Gly		
155	160	165
Pro Val Gly Ser Pro Leu Ser Arg Ile Gly Val Gln Leu Thr Asp		
170	175	180
Ser Ala Tyr Val Val Ala Ser Met Arg Ile Met Thr Arg Leu Gly		
185	190	195
Thr Pro Val Leu Gln Ala Leu Gly Asp Gly Asp Phe Val Lys Cys		
200	205	210
Leu His Ser Val Gly Gln Pro Leu Thr Gly Gln Asp Pro Gly His		
215	220	225
His Gln Pro Cys Arg Glu Glu Ala Leu Cys Gly Ser Arg Leu Pro		

230

235

240

<210> 5
<211> 199
<212> PRT
<213> Homo sapiens

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<400> 5

Met	Glu	Glu	Lys	Thr	Ser	Arg	Ile	Lys	Ala	Ser	Ile	Pro	Gln	Phe
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Thr	Asn	Ser	Pro	Thr	Met	Val	Ile	Met	Val	Gly	Leu	Pro	Ala	Arg
				20				25				30		
Gly	Lys	Thr	Tyr	Ile	Ser	Thr	Lys	Leu	Thr	Arg	Tyr	Leu	Asn	Trp
				35				40				45		
Ile	Gly	Thr	Pro	Thr	Lys	Val	Phe	Asn	Leu	Gly	Gln	Tyr	Arg	Arg
				50				55				60		
Glu	Ala	Val	Ser	Tyr	Lys	Asn	Tyr	Glu	Phe	Phe	Leu	Pro	Asp	Asn
				65				70				75		
Met	Glu	Ala	Leu	Gln	Ile	Arg	Lys	Gln	Cys	Ala	Leu	Ala	Ala	Leu
				80				85				90		
Lys	Asp	Val	His	Asn	Tyr	Leu	Ser	His	Glu	Glu	Gly	His	Val	Ala
				95				100				105		
Val	Phe	Asp	Ala	Thr	Asn	Thr	Thr	Arg	Glu	Arg	Arg	Ser	Leu	Ile
				110				115				120		
Leu	Gln	Phe	Ala	Lys	Glu	His	Gly	Tyr	Lys	Val	Phe	Phe	Ile	Glu
				125				130				135		
Ser	Ile	Cys	Asn	Asp	Pro	Gly	Ile	Ile	Ala	Glu	Asn	Ile	Arg	Gln
				140				145				150		
Val	Lys	Leu	Gly	Ser	Pro	Asp	Tyr	Ile	Asp	Cys	Asp	Arg	Glu	Lys
				155				160				165		
Val	Leu	Glu	Asp	Phe	Leu	Lys	Arg	Ile	Glu	Cys	Tyr	Glu	Val	Asn
				170				175				180		
Tyr	Gln	Pro	Leu	Asp	Glu	Glu	Leu	Asp	Arg	Ser	Ser	Thr	Trp	Ala
				185				190				195		
His	Ala	Thr	Trp											

<210> 6
<211> 406
<212> PRT
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<220>
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<223> Incyte ID No: 7524680CD1

<400> 6

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1	5						10				15			
Tyr	Arg	Arg	Glu	Ala	Val	Ser	Tyr	Lys	Asn	Tyr	Glu	Phe	Phe	Leu
				20				25				30		

Pro Asp Asn Met Glu Ala Leu Gln Ile Arg Lys Gln Cys Ala Leu
 35 40 45
 Ala Ala Leu Lys Asp Val His Asn Tyr Leu Ser His Glu Glu Gly
 50 55 60
 His Val Ala Val Phe Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg
 65 70 75
 Ser Leu Ile Leu Gln Phe Ala Lys Glu His Gly Tyr Lys Val Phe
 80 85 90
 Phe Ile Glu Ser Ile Cys Asn Asp Pro Gly Ile Ile Ala Glu Asn
 95 100 105
 Ile Arg Gln Val Lys Leu Gly Ser Pro Asp Tyr Ile Asp Cys Asp
 110 115 120
 Arg Glu Lys Val Leu Glu Asp Phe Leu Lys Arg Ile Glu Cys Tyr
 125 130 135
 Glu Val Asn Tyr Gln Pro Leu Asp Glu Glu Leu Asp Ser His Leu
 140 145 150
 Ser Tyr Ile Lys Ile Phe Asp Val Gly Thr Arg Tyr Met Val Asn
 155 160 165
 Arg Val Gln Asp His Ile Gln Ser Arg Thr Val Tyr Tyr Leu Met
 170 175 180
 Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys Arg His Gly
 185 190 195
 Glu Ser Glu Leu Asn Ile Arg Gly Arg Ile Gly Gly Asp Ser Gly
 200 205 210
 Leu Ser Val Arg Gly Lys Gln Tyr Ala Tyr Ala Leu Ala Asn Phe
 215 220 225
 Ile Gln Ser Gln Gly Ile Ser Ser Leu Lys Val Trp Thr Ser His
 230 235 240
 Met Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr
 245 250 255
 Glu Gln Trp Lys Ala Leu Asn Glu Ile Asp Ala Gly Val Cys Glu
 260 265 270
 Glu Met Thr Tyr Glu Glu Ile Gln Glu His Tyr Pro Glu Glu Phe
 275 280 285
 Ala Leu Arg Asp Gln Asp Lys Tyr Arg Tyr Arg Tyr Pro Lys Gly
 290 295 300
 Glu Ser Tyr Glu Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met
 305 310 315
 Glu Leu Glu Arg Gln Glu Asn Val Leu Val Ile Cys His Gln Ala
 320 325 330

Val Met Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ser Ser Asp
 335 340 345
 Glu Leu Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu
 350 355 360
 Thr Pro Val Ala Tyr Gly Cys Lys Val Glu Ser Ile Tyr Leu Asn
 365 370 375
 Val Glu Thr Val Asn Thr His Arg Glu Lys Pro Glu Asn Val Asp
 380 385 390
 Ile Thr Arg Glu Pro Glu Glu Ala Leu Asp Thr Val Pro Ala His
 395 400 405

Tyr

<210> 7
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<213> Homo sapiens

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<223> Incyte ID No: 7524757CD1

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Met Glu Glu Lys Thr Ser Arg Ile Lys Ala Ser Ile Pro Gln Phe
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20 25 30
Gly Lys Thr Tyr Ile Ser Thr Lys Leu Thr Arg Tyr Leu Asn Trp
35 40 45
Ile Gly Thr Pro Thr Lys Asp Asn Met Glu Ala Leu Gln Ile Arg
50 55 60
Lys Gln Cys Ala Leu Ala Ala Leu Lys Asp Val His Asn Tyr Leu
65 70 75
Ser His Glu Glu Gly His Val Ala Val Phe Asp Ala Thr Asn Thr
80 85 90
Thr Arg Glu Arg Arg Ser Leu Ile Leu Gln Phe Ala Lys Glu His
95 100 105
Gly Tyr Lys Val Phe Phe Ile Glu Ser Ile Cys Asn Asp Pro Gly
110 115 120
Ile Ile Ala Glu Asn Ile Arg Gln Val Lys Leu Gly Ser Pro Asp
125 130 135
Tyr Ile Asp Cys Asp Arg Glu Lys Val Leu Glu Asp Phe Leu Lys
140 145 150
Arg Ile Glu Cys Tyr Glu Val Asn Tyr Gln Pro Leu Asp Glu Glu
155 160 165
Leu Asp Ser His Leu Ser Tyr Ile Lys Ile Phe Asp Val Gly Thr
170 175 180
Arg Tyr Met Val Asn Arg Val Gln Asp His Ile Gln Ser Arg Thr
185 190 195
Val Tyr Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr
200 205 210
Leu Cys Arg His Gly Glu Ser Glu Leu Asn Ile Arg Gly Arg Ile
215 220 225
Gly Gly Asp Ser Gly Leu Ser Val Arg Gly Lys Gln Tyr Ala Tyr
230 235 240
Ala Leu Ala Asn Phe Ile Gln Ser Gln Gly Ile Ser Ser Leu Lys
245 250 255
Val Trp Thr Ser His Met Lys Arg Thr Ile Gln Thr Ala Glu Ala
260 265 270
Leu Gly Val Pro Tyr Glu Gln Trp Lys Ala Leu Asn Glu Ile Asp
275 280 285
Ala Gly Val Cys Glu Glu Met Thr Tyr Glu Glu Ile Arg Glu His
290 295 300
Tyr Pro Glu Glu Phe Ala Leu Arg Asp Gln Asp Lys Tyr Arg Tyr
305 310 315
Arg Tyr Pro Lys Gly Glu Ser Tyr Glu Asp Leu Val Gln Arg Leu
320 325 330
Glu Pro Val Ile Met Glu Leu Glu